

Figure 1A

1 CCACTGTGCTGGGAATTCGGCACGAGGCGAACGGACGTTTAAAGTGAGAAAAAGAACCGG 60

61 TAAATCAGAGATCCCAGCAAGCGCGTGCATGATAGCGAAGAAAAAGCTATCCG 120

121 TTTCAGTTAACTACTTACCAAGATTGAATTTGCCATCGGGCAAATTACTAAAAATACAT 180

181 AAGTGCAACTCTCCACTGTGTGTGTTTTTTTTTTTTTTTGGTTTTCGCTGTGCC 240

241 TTTATCGCAACAAGAACTGATAAACTAGAAAAATATCTTGAGAAACTGTGTTTCGCGCT 300

301 TTTCTTTTGCTAATTGCCGATCGCGGAAGAGAAAAACAAGCAGTAGACAAAAAAGTGTG 360

361 GTAATACAATCTGAAAAGGGCACCATCAGCAGCCCGAGGGGTTTATCTATATAGATGTCG 420

421 CAGCTTATCATCTCATGCTGTCTGTGAGGTGTTCTGTGTGCTCGTGTAGTATCTTAAAT 480

481 ACATAGAGTGTGTTTCATATAAAGTGCACAAAGCTCGATTGGAACAGCTGTGAGTGCC 540

541 CTTGAGTGGGTGGGCAAGATCGTCATCATCATCATCGTCTCATTATCAACAGAATCAGC 600

601 ATCAGCATCTGGAGGCCCCGGATGCTCTAAGATCCCCAGTGTTCATCAATTATGACTGCC 660

1 M T A 3

661 GAGACCCCTCAAGCCGTTTATAACGCCAACGAGTGCCAACGATGATGGTTTCCGGCCAAA 720

4 E T L K P F I T P T S A N D D G F P A K 23

721 GCGACCAGCACGGCGACCGCCAGCGACGACCCGCGAGCTGATCCCCCTGGTTTGGGG 780

24 A T S T A T A Q R R T R Q L I P L V L G 43

781 TTCATCGGTCTGGGGCTGGTCGTTGCCATTCTCGCACTAACGATCTGGCAGACAACGCGT 840

44 F I G L G L V V A I L A L T I W Q T T R 63

841 GTATCGCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAAATCTCCAGCAG 900

64 V S H L D K E L K S L K R V V D N L Q Q 83

901 CGTTTGGGCATAAACTATCTGGACGAGTTCGACGAGTTCCTCAAAGGAGTACGAGAATGCC 960

84 R L G I N Y L D E F D E F Q K E Y E N A 103

961 CTCATCGACTATCCAAAAAGGTGGATGGCCTCACGGATGAGGAGSACGACGATGGC 1020

104 L I D Y P K K V D G L T D E E D D D D G 123

Figure 1B

1021 GATGGTC⁺TGGATTCCATTGCGGACGACGAGGACGACGACG⁺TTAGCTATAGCTCTGTGGAT 1080
124 D G L D S I A D D E D D D V S Y S S V D 143

1081 GATGTTGGCGCAGACTACGAGGACTACACCGATATGTTAAATAAACTCAACAATGCACAT 1140
144 D V G A D Y E D Y T D M L N K L N N A H 163

1141 ACCGGCACCGCCACATCTGAGACCACTGCTGAGGCGGAGGGCGAGACGGACATGCA 1200
164 T G T T P T S E T T A E G E G E T D S A 183

1201 TCCTCAGCCTCAAATGATGACAATGTGTTGATGACTTTACCAGCTCAGATGCCCTCAA 1260
184 S S A S N D D N V F D D F T S S D A L K 203

1261 AAGAAGCAGGAGAGAAAAATCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATT 1320
204 K K Q E R K S R S I A D V R N E E Q N I 223

1321 CAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAGCTTCCAAAGAGAGC 1380
224 Q G N H T E L Q E K S S N E A A S K E S 243

1381 CCTGCAGCACTTCACCTCCGTGCGAGAATGCATTCGCCCATCGCCACCTCGTAGTCCGC 1440
244 P A A L H L R R R M H S R H R H L V V R 263

1441 AAAGCCAGATCCGAGGACTCGAGGCCAGCAGCCCAATTCCACTTGAGCAGCAGGCGGCGT 1500
264 K A R S E D S R P A A H F H L S S R R R 283

1501 CACCAAGAAAGTATGGGCTACCATGGAGATATGTACATAGAAAATGATAGGAGAGATGC 1560
284 H Q E S M G Y H G D M Y I E N D R E R C 303

1561 TCTTATCAGGGACACTTTCAAACGCGCATGGCGTATTGACGGTGACCAATGCAGGCCTA 1620
304 S Y Q G H F Q T R D G V [REDACTED] 323

1621 TATTACGTATACGCCCAGATATGGGGCTACAACCTCGCAGCAGACGAGAACGGATTTATCGTC 1680
324 [REDACTED] G Y N S H D Q N G F I V 343

1681 TTTCAAGGAGACACTCCATTCCGTGAGTGCTTGAACACGGTGCCCAACAACATGCCACAT 1740
344 F Q G D T P F L Q C L N T V P T N M P H 363

1741 AAGGTGCACACCTGCCACACGAGTGGTCTGATCCACCTGGAACGAAACAGAGGATCCAT 1800
364 K V H T C H T S G L I H L E R N E R I H 383

1801 CTGAAGGACATTACAACGATCGCAATGCAGTTCTGCGGGAGGGAAACAACCGAAGCTAC 1860
384 L K D I H N D R N A V L R E G N N R S Y 403

Figure 1C

1861 TTTGGCATCTTCAAGGTGTAAATTGGAGAGATTATCCCCGGTCAGAAGATGGAATACCAG 1920
404 F G I F K V 409

1921 TTTAAGCTTTTGTCCCCGCGACTGCTCGTGAAATGCGATTTCATCGCCAGCGTGAATCCATT 1980

1981 AGTTCGTAGTACCTAGTCTTAGTCACTCCAAACCTAATCTCAATCGGAATCGTGCATACT 2040

2041 GCATTAGTCAGAAGACGGAGGAAAAATCATATTTATTTTGTATATACTCGTTCGACTCTAA 2100

2101 AAAGTGAATAAAAAATATATGTAGCTATTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAC 2160

2161 CTCGAG 2166

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Figure 2A

1	ATGACTGCCGAGACCCCTCAAGCCGTTTATAACGCCAACGAGTGCCAACGATGATGGTTT	60
1	<u>M T A E T L K P F I T P T S A N D D G F</u>	20
61	CCGGCCAAAGCGACCGACGCGGACCGCCGACGACGCCGCGAGCTGATCCCCCTG	120
21	<u>P A K A T S T A T A Q R R T R Q L I P L</u>	40
121	GTTTGGGGTTCATCGGTCTGGGGCTGGTTCGTCATTCTCGCACTAACGATCTGGCAG	180
41	<u>V L G F I G L G L V V A I L A L T I W Q</u>	60
181	ACAACCGGTGTATCGCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTTCGTCGATAAT	240
61	T T R V S H L D K E L K S L K R V V D N	80
241	CTCCAGCAGCGTTTGGGCATAAACTATCTGGACGAGTTCGACGAGTTCGAAAAGGAGTAC	300
81	L Q Q R L G I N Y L D E F D E F Q K E Y	100
301	GAGATGCCCTCATCGACTATCCAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGAC	360
101	E N A L I D Y P K K V D G L T D E E D D	120
361	GACGATGGCGATGGTCTGGATTCCATTGCGGACGACGAGGACGACGACGTTAGCTATAGC	420
121	D D G D G L D S I A D D E D D D V S Y S	140
421	TCTGTGGATGATGTTGGCGCAGACTACGAGGACTACACCGATATGTTAAATAAACTCAAC	480
141	S V D D V G A D Y E D Y T D M L N K L N	160
481	AATGCACATACCGGCACCGCCACATCTGAGACCCTGCTGAGGGCGAGGGCGAGAGC	540
161	N A H T G T T P T S E T T A E G E G E T	180
541	GACAGTGCATCCTCAGCCTCAAATGATGACAATGTGTTTCGATGACTTTACCAGCTACAAT	600
181	D S A S S A S N D D N V F D D F T S Y N	200
601	GCCCCAAAAAGAAGCAGGAGAGAAAATCTCGCTCGATTGCCGATGTACGCAATGAGGAG	660
201	A H K K K Q E R K S R S I A D V R N E E	220
661	CAGAATATCAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAAATGAGGCAACTTCC	720
221	Q N I Q G N H T E L Q E K S S N E A T S	240
721	AAAGAGAGAATGCATTCGCGCCATCGCCACCTCCTAGTCCGCAAAGGTGAATCTCTCTTT	780
241	K E R M H S R H R H L L V R K G E S L L	260
781	TCAGCCAGATCCGAGGACTCGAGGCCAGAGCCCATTTCCACTTTCGAGCAGCAGGCGGCGT	840
261	S A R S E D S R P A A H F H L S S R R R	280
841	CACCAAGGAAGTATGGGCTACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAAC	900
281	H Q G S M G Y H G D M Y I G N D N E R N	300

Figure 2B

901 TCTTATCAGGGACACTTTCAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTA 960
301 S Y Q G H F Q T R D G V [REDACTED] 320

961 TATTACGTATACGCCAGATATGCTACAACAACCTCGCAGACCAGAACGGATTATCGTC 1020
321 ██████████ N N S H D O N G F I V 340

1021 TTTCAAGGAGACACTCCATTCTGCAGTGTCTGAACACGGTGCCCAACATGCCACAT 1080
341 F Q G D T P F L Q C L N T V P T N M P H 360

1081 AAGGTGCACACCTGCCACACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCAT 1140
361 K V H T C H T S G L I H L E R N E R I H 380

1141 CTGAAGGACATTCAACGATCGCAATGCAGTTCTGCGGGAGGGAAACAACCGAAGCTAC 1200
381 L K D I H N D R N A V L R E G N N R S Y 400

1201 TTTGGCATCTTCAAGGTGTAA 1221
401 F G I F K V 406

Figure 3A

1 GGCACGAGGCGAACGGACGCTTTAAAGTGAGAAAAGAAACCGGTAAATCAGAGATCCCAAG 60

61 CAAGCGCGTCGTCGATGATAGCGAAGAAAAAGCTATCCGTTTCAGTTAACTACTTAC 120

121 CAAGATTGAATTCGCCATCGGGCAAATTACTAAAAATACATAAGTGCAACTCGTCCACT 180

181 GTGTGTGTGTTTTTTTTTTTTTTTGGTTTTTCGCTGTGCCTTTATCGCAAACAAGAAC 240

241 TGATAAACTAGAAAAATATCTTGAGAAACTTGTTTTTCGCGCTTTTCTTTTGCTAATTGCC 300

301 GATCGCGGAAGAGAAAAACAAGCAGTAGACAAAACAAGTGTGGTAATACAATCTGAAAAG 360

361 GGCACCATCAGCAGCCCGAGGGGTTTATCTATATAGATGTGCGAGCTTATCATCTCATGC 420

421 TGTCTGTGAGGTTGTTCTGTGTGCTCGTGTATATCTTAAATACATAGAGTGTGTTCTATA 480

481 TAAAGTGCACAAAGCTCGATTGGAAACAGCTGTCGAGTGCCTTGAGTGGTGGGCAAG 540

541 ATCGTCATCATCATCATCGTCGTCAATTATCAACAGAATCAGCATCAGCATCTGGAGGCC 600

601 CGGTTGCTCTAAGATCCCCAGTGTTTCATCAATTATGACTGCCGAGACCTCAAGCCGTTT 660

1 M T A E T L K P F 9

661 ATAACGCCAACGAGTGCCAAACGATGATGGTTTTTCGCGCCAAAGCGACACGCGCGACC 720

10 I T P T S A N D D G F P A K A T S T A T 29

721 GCCCAGCAGCGCACCCCGCAGCTGATCCCCCTGGTTTTTGGGGTTTCATCGGTCTGGGGCTG 780

30 A Q R R T R Q L I P L V L G F I G L G L 49

781 GTCGTTGCCATTCTCGCACTAACGATCTGGCAGACACGCGTGTATCGCATCTGGACAAG 840

50 V V A I L A L T I W Q T T R V S H L D K 69

841 GAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTTGGGCATAAACTAT 900

70 E L K S L K R V V D N L Q Q R L G I N Y 89

901 CTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCATCGCATATCCAAA 960

90 L D E F D E F Q K E Y E N A L I D Y P K 109

961 AAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGGTCTGGATTCCATT 1020

110 K V D G L T D E E D D D D G D G L D S I 129

Figure 3B

1021 GCGGACGACGAGGACGACGACGTTAGCTATAGCTCTGTGGATGATGTTGGCGCAGACTAC 1080
130 A D D E D D D V S Y S S V D D V G A D Y 149

1081 GAGGACTACACCGATATGTTAAATAAACTCAACAATGCACATACCGGCACCAGCCCCACA 1140
150 E D Y T D M L N K L N N A H T G T T P T 169

1141 TCTGAGACCACTGCTGAGGGCGAGGGCGAGACGACAGTGCATCCTCAGCCTCAAATGAT 1200
170 S E T T A E G E G E T D S A S S A S N D 189

1201 GACAAATGTGTTTCGATGACTTTACCAGCTACAATGCCCCACAAAAGAAGCAGGAGAGAAAA 1260
190 D N V F D D F T S Y N A H K K K Q E R K 209

1261 TCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATTCAAGGAAATCACACAGAG 1320
210 S R S I A D V R N E E Q N I Q G N H T E 229

1321 CTTACGAGAAAAGTCATCCAAATGAGGCAACTTCCAAGAGAGCCCTGCACCACTTCACCAC 1380
230 L Q E K S S N E A T S K E S P A P L H H 249

1381 CGTCGCAGAATGCATTCCCGCCATCGCCACCTCCTAGTCCGCAAAGCCAGATCCGAGGAC 1440
250 R R R M H S R H R H L L V R K A R S E D 269

1441 TCGAGGCCAGCAGCCCAATTTCCACTTGAGCAGCAGGCGGCGTCACCAAGGAAGTATGGGC 1500
270 S R P A A H F H L S S R R R H Q G S M G 289

1501 TACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAACTCTTATCAGGACACTTTT 1560
290 Y H G D M Y I G N D N E R N S Y Q G H F 309

1561 CAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCCAG 1620
310 Q T R D G V [REDACTED] 329

1621 ATATGCTACAACAACTCGCACGACCCAGAACGGATTTATCGTCTTTCAAGGAGACACTCCA 1680
330 [REDACTED] N N S H D Q N G F I V F Q G D T P 349

1681 TTCTGCAGTGCTTGAACACGGTGCCCCACCAACATGCCACATAAGGTGCACACCTGCCAC 1740
350 F L Q C L N T V P T N M P H K V H T C H 369

1741 ACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCATCTGAAGGACATTCACAAC 1800
370 T S G L I H L E R N E R I H L K D I H N 389

1801 GATCGCAATGCAGTTCTCGGGGAGGGAACAACCGAAGCTACTTTGGCATCTTCAAGGTG 1860
390 D R N A V L R E G N N R S Y F G I F K V 409

1861 TAAATGGAGAGATTATCCCCGGTCAGAAGATGGAATACCAGTTTAAGCTTTTGTCCTCCG 1920

Figure 3C

1921 CGACTGCTCGTGAATGCGATTCA[.]TCGCCAGCGTGAATCCATTAGTTCGTAGTACCTAGTC 1980
1981 TTAGTCACTCCAAACCTAATCTCAATCGGAATCGTGCATACTGCATTAGTCAGAAGACGG 2040
2041 AGGAAAAATCATATTTATTTGTATATACTCGTTCGACTCTAAAAAGTGAATAAAATATA 2100
2101 TGTAGCTATTAAAAA[.]AAAAAAAAAAAAAAAAAAAAAAAAAAAACTCGAG 2148

1921
1981
2041
2101
2148

Figure 4

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1                               50
DnTNF (1) YTAETLKPFITPTPSANDDGFPAKATSTATAQRRTQLIPLVLGPIGLGLV
DnTNFv1 (1) YTAETLKPFITPTPSANDDGFPAKATSTATAQRRTQLIPLVLGPIGLGLV
DnTNFv2 (1) YTAETLKPFITPTPSANDDGFPAKATSTATAQRRTQLIPLVLGPIGLGLV

51                               100
DnTNF (51) VAILALTWQITRVSHLDKELSLKRWVDNLQQRIGINYLDFFDPEQKEY
DnTNFv1 (51) VAILALTWQITRVSHLDKELSLKRWVDNLQQRIGINYLDFFDPEQKEY
DnTNFv2 (51) VAILALTWQITRVSHLDKELSLKRWVDNLQQRIGINYLDFFDPEQKEY

101                              150
DnTNF (101) ENALIDYPRKVDGLIDDEEDDCCDGLDSTADCEDDDVSYSSVDVQADYE
DnTNFv1 (101) ENALIDYPRKVDGLIDDEEDDCCDGLDSTADCEDDDVSYSSVDVQADYE
DnTNFv2 (101) ENALIDYPRKVDGLIDDEEDDCCDGLDSTADCEDDDVSYSSVDVQADYE

151                              200
DnTNF (151) DYTDLNLKLNIAHTTPTTSETTAARGEGETDSASSASNDENVFDDPTS
DnTNFv1 (151) DYTDLNLKLNIAHTTPTTSETTAARGEGETDSASSASNDENVFDDPTS
DnTNFv2 (151) DYTDLNLKLNIAHTTPTTSETTAARGEGETDSASSASNDENVFDDPTS

201                              250
DnTNF (201) AKKKQERKRSSTADVRNEECNIQCNHTLEQKSSNEAFSKFSPAALHLR
DnTNFv1 (201) AKKKQERKRSSTADVRNEECNIQCNHTLEQKSSNEAFSKFS
DnTNFv2 (201) AKKKQERKRSSTADVRNEECNIQCNHTLEQKSSNEAFSKFS

251                              300
DnTNF (251) KRHSRHRRLVRR-----ARSDSRPAAHFLSSRRRHQSMGYHGLD
DnTNFv1 (243) KRHSRHRRLVRRGBSLLSARSDSRPAAHFLSSRRRHQSMGYHGLD
DnTNFv2 (251) KRHSRHRRLVRR-----ARSDSRPAAHFLSSRRRHQSMGYHGLD

301                              350
DnTNF (295) YLENDNERSYVQGHFQTRDGLVITVINGLYYYVYAOICWNNSHDQNGFIVE
DnTNFv1 (292) YLENDNERSYVQGHFQTRDGLVITVINGLYYYVYAOICWNNSHDQNGFIVE
DnTNFv2 (295) YLENDNERSYVQGHFQTRDGLVITVINGLYYYVYAOICWNNSHDQNGFIVE

351                              400
DnTNF (345) AGDITFFQLQINWPTNNPRKVVHTCHTSLIHLERNRERHLKQTHNDRNAY
DnTNFv1 (342) AGDITFFQLQINWPTNNPRKVVHTCHTSLIHLERNRERHLKQTHNDRNAY
DnTNFv2 (345) AGDITFFQLQINWPTNNPRKVVHTCHTSLIHLERNRERHLKQTHNDRNAY

401                              415
DnTNF (395) LREGNNRSYFGIFKV
DnTNFv1 (392) LREGNNRSYFGIFKV
DnTNFv2 (395) LREGNNRSYFGIFKV

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Figure 5

AC005974 : DS05033 (P1 D347), DS01913 (P1 D350). Finished; 158983 bases.
Length = 158,983

Minus Strand HSPs:

Score = 77 (27.1 bits), Expect = 5.5, P = 1.0
Identities = 20/58 (34%), Positives = 31/58 (53%), Frame = -1

Query: 203 NGKLI**VNQDGFYLYANIC**FRH-HETSGDLA---TEYQLQMLVYV-TKTSIKIPSSHT 254
+G L V G YY+YA IC+ + H+ +G + T +LQ + V T K+ + HT
Sbjct: 129394 DGVLT**VNTGLYVYAQIC**YNNSHDQNGFIVPQGDTPFLQCLNTVPTNMPHKVHTCHT
129221

Score = 45 (15.8 bits), Expect = 79., Sum P(2) = 1.0
Identities = 9/17 (52%), Positives = 10/17 (58%), Frame = -1

Query: 28 GELHAPP--PPAPHQPP 42
GP PP PP+P PP
Sbjct: 132361 GFSLPFPFPFPFSPRTFP 132311

Figure 6A

		1	50
DmTNF	(1)	--MTAETLPPPTPTSTANDGFPKATSTSTAQOR-----	
DmTNFv1	(1)	--MTAETLPPPTPTSTANDGFPKATSTSTAQOR-----	
DmTNFv2	(1)	--MTAETLPPPTPTSTANDGFPKATSTSTAQOR-----	
Osteoprotegerin	(1)	-----MRRASRDYTKYLRSSSEEMGGGPGAPIHEGLHAPPPPPA	
hCD27L	(1)	-----	
hCD30L	(1)	-----	
hTRAIL	(1)	-----MAMMENQSGP-----	
hEctodysplasmin_A	(1)	MGYPEVERRELPAAAPRRRCSCGCGCGAPARA-----	
mEctodysplasmin_A	(1)	MGYPEVERRELPAAAPRRRCSCGCGCGAPARA-----	
		51	100
DmTNF	(33)	---RTRGLIPIVLGHISGLVVAITLITITOTTTRSHLDKELKSDRVV	
DmTNFv1	(33)	---RTRGLIPIVLGHISGLVVAITLITITOTTTRSHLDKELKSDRVV	
DmTNFv2	(33)	---RTRGLIPIVLGHISGLVVAITLITITOTTTRSHLDKELKSDRVV	
Osteoprotegerin	(39)	HQPPAASRSMFVALGLGLHGVVCSVALFFMFRACMDPN-----RISE	
hCD27L	(1)	-----	
hCD30L	(1)	-----	
hTRAIL	(11)	---SLGGTCVLIUHTVVLQSLCNAVTVVFTNEM-----KQM	
hEctodysplasmin_A	(35)	---GEGNSCLPLGFGGLSLAHHLATCCCKLELRS-----EERER	
mEctodysplasmin_A	(35)	---GEGNSCLPLGFGGLSLAHHLATCCCKLELRS-----EERER	
		101	150
DmTNF	(79)	DNLQQRLLSYNYLDEFDEFQKEYENALIDYPKVGLDTDEDDDGDGLDS	
DmTNFv1	(79)	DNLQQRLLSYNYLDEFDEFQKEYENALIDYPKVGLDTDEDDDGDGLDS	
DmTNFv2	(79)	DNLQQRLLSYNYLDEFDEFQKEYENALIDYPKVGLDTDEDDDGDGLDS	
Osteoprotegerin	(82)	DGTHCIYR-----ILRLHNDFQITTLSSQDT---	
hCD27L	(1)	-----	
hCD30L	(1)	-----	
hTRAIL	(47)	DKYSKS---G-----TACFLAEDDSYMDPNDIES-	
hEctodysplasmin_A	(73)	GAESRLCGSGTPGTSGTLLSLGGLDDPSPIITHLQPSFQQLPEESAA	
mEctodysplasmin_A	(73)	GAESRLCGSGAPGTSGTLLSSPGSLDPVGPITHLQPSFQQLPEESDP	
		151	200
DmTNF	(129)	TADDEDVDVSYSSYDDVGADYEDVDMLNLNNAHGTTPTSETTTCGEG	
DmTNFv1	(129)	TADDEDVDVSYSSYDDVGADYEDVDMLNLNNAHGTTPTSETTTCGEG	
DmTNFv2	(129)	TADDEDVDVSYSSYDDVGADYEDVDMLNLNNAHGTTPTSETTTCGEG	
Osteoprotegerin	(110)	-----KLIPDSRRIRKQAFQGAQKELCHIVGSOQHIAE	
hCD27L	(1)	-----MPBEGSCSRRRPYGCVLRAILVPL	
hCD30L	(1)	-----MDPLQQAALNGMPPGDTAMHVPAASVAS	
hTRAIL	(73)	-----MN--SPGVVWQLRQLRRMLIRTSSETTITVQ	
hEctodysplasmin_A	(123)	DHSSCGHQMILINFFFPPEKATSEESER--LRNKRKSGEGECPV	
mEctodysplasmin_A	(123)	DPPSCRHQMILINFFFPPEKATSEESER--LRNKRKSGEGECPV	
		201	250
DmTNF	(179)	ETD-SASSASNDNVDFDFTSYNAHKKQERKSRSDADRNNEQNQCNIH	
DmTNFv1	(179)	ETD-SASSASNDNVDFDFTSYNAHKKQERKSRSDADRNNEQNQCNIH	
DmTNFv2	(179)	ETD-SASSASNDNVDFDFTSYNAHKKQERKSRSDADRNNEQNQCNIH	
Osteoprotegerin	(144)	KAWVDG-----SWLDAK	
hCD27L	(27)	VAG-----LVLCIVCIQR	
hCD30L	(30)	HLGTSRSYFYLTATLALCLVFTVATIMVLVVGQTDSPN-----	
hTRAIL	(105)	EKKQ-----NRPVVR	
hEctodysplasmin_A	(171)	KNK-KKGGKGGPPGPGNGPPGPPGPGQPGPIPGIPQIPG--TTVMPP	
mEctodysplasmin_A	(171)	KNK-KKGGKGGPPGPGNGPPGPPGPGPGQPGPIPGIPG--TTVMPP	
		251	300
DmTNF	(228)	TELQEKSSNEAASKESPAALHLRRMRSHRHVLVVRK-----ARSDSR	
DmTNFv1	(228)	TELQEKSSNEAASKESPAALHLRRMRSHRHVLVVRK-----ARSDSR	
DmTNFv2	(228)	TELQEKSSNEAASKESPAALHLRRMRSHRHVLVVRK-----ARSDSR	
Osteoprotegerin	(157)	-----RSKDEAP	
hCD27L	(41)	-----FAGACQQPLES	
hCD30L	(71)	-----SDNVPLKGCN-----CSED	
hTRAIL	(116)	---ERGP-----RVAALITIT	
hEctodysplasmin_A	(218)	GPPGPPGPGPPGPGIQQP-----GAADAKTIT-----ENQP	
mEctodysplasmin_A	(218)	GPPGPPGPGPPGPGIQQP-----GAADAKTIT-----ENQP	

Figure 6B

		301				350
	DmTNF	(272)	PAAEFHLSSRRRHQGS	MGYHCDMYIENDRER-C	SYQGHEQTQDGV	IVITN
	DmTNFv1	(269)	PAAEFHLSSRRRHQGS	MGYHCDMYIGNDNER-N	SYQGHEQTQDGV	IVITN
	DmTNFv2	(272)	PAAEFHLSSRRRHQGS	MGYHCDMYIGNDNER-N	SYQGHEQTQDGV	IVITN
	Osteoprotegerin	(165)	--FAHLTINATDIPSG-SHKVSL	SSWYVDRG-WAKESNMFTSNC	SLITNQ	
	hCD27L	(53)	--LGWDVALQLNHTGP	QQDPRLVWQGGPALGR	SPFHGPELKKCOLRIHR	
	hCD30L	(86)	LLCILKRAPPFKKSWAYL	QVAKHDKTKLSWNKDS	ELHGVRYQDCAVYQF	
	hTRAIL	(131)	-GRSN-TLSSPNSKNEKALGR	KINSWESSRSGHSGNSNLHLR	NCDEVTHE	
	hEctodysplasmin_A	(249)	AVVLLQGGGSAIQVKNL	SGGVNDWSRITM-NRKKFKLHP	SPCELVLV	
	mEctodysplasmin_A	(249)	AVVLLQGGGSAIQVKNL	SGGVNDWSRITM-NRKKFKLHP	SPCELVLV	
		351				400
	DmTNF	(321)	AGHYNY-----	AQEWGYSHQNGEIVHQG-IT	PFLOCNNEVFNPM	
	DmTNFv1	(318)	TCHYNY-----	AQCYNYSHQNGEIVHQG-IT	PFLOCNNEVFNPM	
	DmTNFv2	(321)	TCHYNY-----	AQCYNYSHQNGEIVHQG-IT	PFLOCNNEVFNPM	
	Osteoprotegerin	(211)	DEHYTYANICFRHHETSGD	LATEYLQLVYTKTKIKPSSHTL	MKGGS	
	hCD27L	(101)	DSHYTHVLCVTLAICSST	TASRHHPTLALGICS--	IASSSLSLRLSF	
	hCD30L	(136)	PSHYFLICLQLFLVQC	PNNVDLKLLELNKHIKKQ	ALVTVESEHOKKH	
	hTRAIL	(179)	KSEYVLYSGTYPRFQEE	KENTKNKQMVQVYLYK-YT	SPFPLMLLKEAR	
	hEctodysplasmin_A	(298)	DSHYFLVSG-----	VEYYINFTFASMEVVD-EP	PFLOCNTRSLITGK	
	mEctodysplasmin_A	(298)	DSHYFLVSG-----	VEYYINFTFASMEVVD-EP	PFLOCNTRSLITGK	
		401				450
	DmTNF	(362)	PHK-----	VHCHTSGLIHERNEE	EHRTTHNDRNAVIREGNNR	SY
	DmTNFv1	(359)	PHK-----	VHCHTSGLIHERNEE	EHRTTHNDRNAVIREGNNR	SY
	DmTNFv2	(362)	PHK-----	VHCHTSGLIHERNEE	EHRTTHNDRNAVIREGNNR	SY
	Osteoprotegerin	(261)	TKYWSGNSEFHFYS	INVCQFFKURSGEES	SEVSNPSLDPDQ---DAEY	
	hCD27L	(148)	HQG-----	CLVSQRTPARGDECT	RLTGTLPSRNT---DETH	
	hCD30L	(186)	VYQN-----	LSQFLDYVQNTTHSN	MDTFYIDTSTFPLEN	ZE
	hTRAIL	(228)	NSCWSKDAEYGL	RYTCCGHPFKENDRHF	VEVTEVNEHEDMDH---	EASE
	hEctodysplasmin_A	(341)	TN-----	YNTCTAGVCLIKARQK	LAURVAFASINSGS--	KHTTE
	mEctodysplasmin_A	(341)	TN-----	YNTCTAGVCLIKARQK	LAURVAFASINSGS--	KHTTE
		451				462
	DmTNF	(404)	FCGEEV-----			
	DmTNFv1	(401)	FCGEEV-----			
	DmTNFv2	(404)	FCGEEV-----			
	Osteoprotegerin	(308)	FCAGVDRDID--			
	hCD27L	(186)	FCVCMWRP----			
	hCD30L	(226)	SIFVYSNSD---			
	hTRAIL	(275)	FCAGLVG-----			
	hEctodysplasmin_A	(380)	FCATKGEAPAS			
	mEctodysplasmin_A	(380)	FCATKGEAPAS			

Figure 7

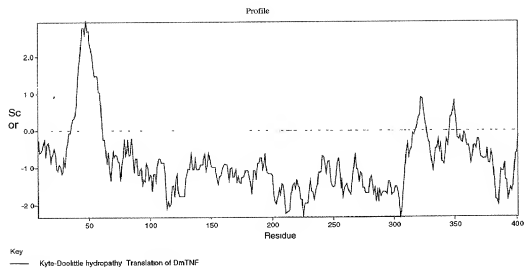


Figure 8

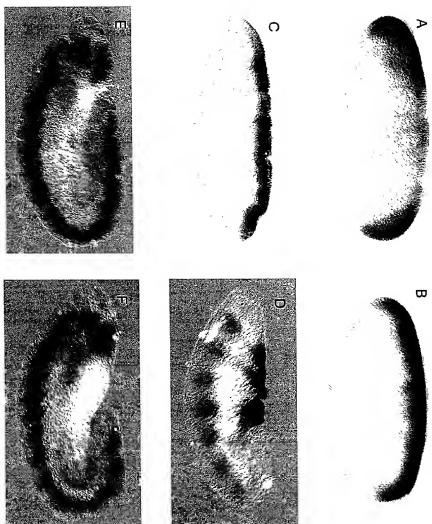
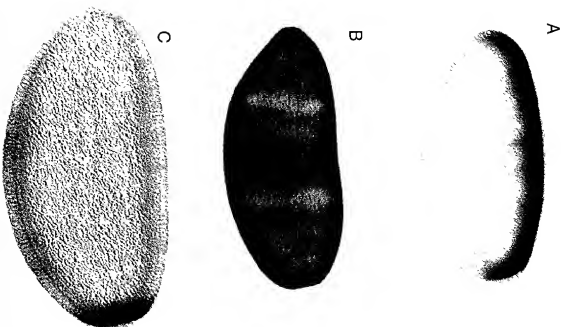


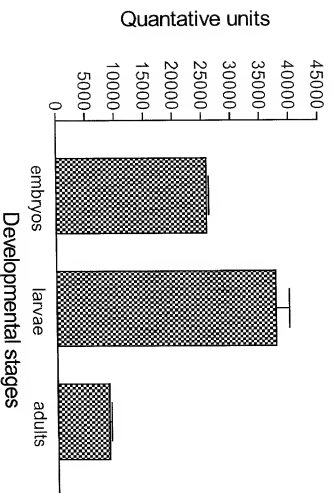
Figure 9



00000000.00000000

Figure 10

Expression profile of *Drosophila* TNF during development



000433250.022004

Figure 11

DmTNF

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human osteoprotegerin protein	gil12643360	21.4%	35.7%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	24.6%	34.4%
human ectodysplasmin_A protein	gilQ92838	21.2%	27.9%
mouse ectodysplasmin_A protein	gilNP_034229	20.4%	28.5%

DmTNFv1

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human osteoprotegerin protein	gil12643360	23.8%	30.5%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	23.3%	32.7%
human ectodysplasmin_A protein	gilQ92838	21.8%	28.6%
mouse ectodysplasmin_A protein	gilNP_034229	21%	28.6%

DmTNFv2

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human osteoprotegerin protein	gil12643360	21.4%	35.7%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	24.1%	33.9%
human ectodysplasmin_A protein	gilQ92838	22.4%	29.1%
mouse ectodysplasmin_A protein	gilNP_034229	21.6%	29.2%

Figure 12

